

LOCUS BG529820 826 bp mRNA linear EST 03-APR-2001
 DEFINITION 602558904F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4696752 5',
 mRNA sequence.
 ACCESSION BG529820
 VERSION BG529820.1 GI:13521357
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 826)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1524 row: h column: 01
 High quality sequence stop: 820.

FEATURES Location/Qualifiers
 source 1..826
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4696752"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_61"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 44.8%; Score 733.6; DB 12; Length 826;
 Best Local Similarity 97.6%; Pred. No. 3.5e-161;
 Matches 798; Conservative 0; Mismatches 14; Indels 6; Gaps 5;

Qy 1 GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCT 60
 |||||
 Db 11 GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCT 70
 Qy 61 GACACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCTTCTCTGTGGTTTGCTGGCAGC 120

Db	71		GACACCTGGGAAGATGGCCGGCCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGC	130
Qy	121		CACCTTGATCCAAGCCACCCCTCAGTCCCCTGAGTTCTCATCCTCGGCCCAAAGTCAT	180
Db	131		CACCTTGATCCAAGCCACCCCTCAGTCCCCTGAGTTCTCATCCTCGGCCCAAAGTCAT	190
Qy	181		CAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCT	240
Db	191		CAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCT	250
Qy	241		GCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT	300
Db	251		GCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT	310
Qy	301		GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCA	360
Db	311		GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCA	370
Qy	361		GCTGCAGGTGAAGCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACAT	420
Db	371		GCTGCAGGTGAAGCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACAT	430
Qy	421		GGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGA	480
Db	431		GGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGA	490
Qy	481		GGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCCTCAG	540
Db	491		GGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCCTCAG	550
Qy	541		TGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTATAAGCTCTCCTTCCT	600
Db	551		TGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTATAAGCTCTCCTTCCT	610
Qy	601		GGTGAACGCCTT-AGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAG	659
Db	611		GGTGAACGCCTTAAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAG	670
Qy	660		TGAAAAACCAGCTGTGTCCC--GTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCT	717
Db	671		TGAAAAACCAGCTGTGTCCCCGTGAATCGAGGCTTCCTTCAATGGCATGTATGCAGACCT	730
Qy	718		-CCTGCAGCTGGTGAAGGTGCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTC	776
Db	731		CCCTGCAGCTGGTGAAGGTGCCATTTCCCTCAGCATTGACCG-CTGGAGTTGGACCTTC	789
Qy	777		TGTATCCTGCCATCAAGGGTGACACCATTAGCTCTAC	814
Db	790		TTGTATCTGCCATC-AGGGTGACCCCATTCAGTTCTAC	826